

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/691,763A

DATE: 03/22/2001
 TIME: 16:22:00

Input Set : A:\E03557003NEW.TXT
 Output Set : N:\CRF3\03222001\I691763A.raw

ENTERED

4 <110> APPLICANT: Vertino, Paula M.
 6 <120> TITLE OF INVENTION: TMS1 Compositions and Methods of Use
 9 <130> FILE REFERENCE: E0355/7003/ERG/MAT
 11 <140> CURRENT APPLICATION NUMBER: US 09/691,763A
 12 <141> CURRENT FILING DATE: 2000-10-18
 14 <150> PRIOR APPLICATION NUMBER: US 60/159,975
 15 <151> PRIOR FILING DATE: 1999-10-18
 17 <160> NUMBER OF SEQ ID NOS: 27
 19 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 2821
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo Sapiens
 26 <400> SEQUENCE: 1

| | | | | | | | |
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| 27 | aagcttttga | atacaacatg | ctgcaggcat | cacagcctca | ttcattcctt | cactcagcaa | 60 |
| 28 | atcttttact | agcaccta | gtgttccaga | tacatttttt | tttttcagat | ggaatctagc | 120 |
| 29 | tctgtcacc | aggtcgag | gcagtggtgc | aatcttggt | cactgtagcc | tctgcctccg | 180 |
| 30 | aggttcaag | gatttctat | cctcagccgc | cctagtagct | aggattacag | gcgcccctca | 240 |
| 31 | ccacacacag | ctatttccag | gtacattctt | gacgctagga | attcagcaaa | gaataagaca | 300 |
| 32 | gttaaggct | ccgatgctca | taggcctcac | attttagaga | gggatgaatg | tccaataagc | 360 |
| 33 | atataaacat | ataatatgtc | agggtcgtat | gactacaagg | aacagtgatt | gttacaaacc | 420 |
| 34 | agatgagagg | gaaaaataaa | ggattccaaa | tatccccctt | gggaagtaga | gtcaggattc | 480 |
| 35 | aaacaaagaa | ctgtatggct | tcaagttcat | ggtctttaat | ctcctggagg | ctgtctctct | 540 |
| 36 | ttcttttttc | ttttttttaa | tcagtgttgg | gatcaaattc | tggctcccct | aggaagcacc | 600 |
| 37 | tggcaagggt | tcgggagcca | tcgggttggc | catgttatgc | tggaaatatt | ataagcaccc | 660 |
| 38 | gagggttatc | cccatgtcgt | agaaaatgaa | actgaagctc | agagagattt | gcactctctg | 720 |
| 39 | ccctttttgt | caactcattt | ttccccagta | tgtggaattg | agggagcttc | acgtctctag | 780 |
| 40 | ctgtcatgat | tccaagattc | tacgacatgt | gggagaggat | cctaagggtt | ggggaaccgc | 840 |
| 41 | ggagggttct | gggttctaga | aatccgaggt | tctaagccta | ggtgctccaa | taaaccacgt | 900 |
| 42 | gagagccagc | ccaggtttcc | ggtctgtacc | cgctgggtgc | agcccagaga | caagcaggcg | 960 |
| 43 | ccacccatga | gccccctctg | ggccccctcc | cggttcccac | ctcgcaggcc | agctggaggg | 1020 |
| 44 | cgcgatcctg | cgctcccccg | acggcctggg | gccccaatcc | agaggcctgg | gtgggagggg | 1080 |
| 45 | accaaggggt | tagtaaggaa | gcgccttttg | ctggagggca | acggaccggg | gcggggagtc | 1140 |
| 46 | gggagaccag | agtgaggagg | agggggggag | tccagggttc | gccccggagc | cgacttcttc | 1200 |
| 47 | ctggctggcg | gctgcagcgg | ggtgagcggc | ggcagcggcc | ggggatcctg | gagccatggg | 1260 |
| 48 | gcgcgcgcgc | gacgccatcc | tggatgcgct | ggagaacctg | accgccgagg | agctcaagaa | 1320 |
| 49 | gttcaagctg | aagctgctgt | cggtgcccgt | gcgcgagggc | tacgggcgca | tcccgcgggg | 1380 |
| 50 | cgcgctgctg | tccatggacg | ccttggaact | caccgacaag | ctggtcagct | tctacctgga | 1440 |
| 51 | gacctacggc | gcccagatca | ccgctaactg | gctgcgcgac | atgggcctgc | aggagatggc | 1500 |
| 52 | cgggcagctg | caggcgccca | cgcaccaggg | tgagccgcgc | ccgttcccct | ccaccccgtc | 1560 |
| 53 | tttccccctc | acccacacca | gcgcttacc | cgcgggctct | tccgctttct | gttctctcta | 1620 |
| 54 | ccccataaca | aagctgctct | accggaaagg | aggctcccca | cgcttgccct | accgaccaac | 1680 |
| 55 | gggaccccgg | ccccacggcg | ggaagggaag | ggaaggggat | cacttgcccc | atatcttctc | 1740 |
| 56 | aggtctctga | gcgcgcgcag | ctgggatcca | ggccccctct | cagtcggcag | ccaagccagg | 1800 |
| 57 | tgaggcctcc | acacccagcc | cggccccacc | gcactcctgc | acagcctgca | tctgtgctcc | 1860 |
| 58 | cgcaaccagg | gcagggcagg | gcagggcagg | cacggcttgg | caacctgcgc | caccccaccc | 1920 |
| 59 | accaaccac | accctgcggg | ggaaggggaga | caatattacc | ctcatccacc | tgcattgtgg | 1980 |

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60 gtcctggtgg ccgcccctg gagccctgcc cctaggcttg cagaggaatt cctgaagaac 2040
61 tcaagttcag cagggacagg cccacacccc tggctgctgg ctcatgttct cctcccaccc 2100
62 ccaggcctgc actttataga ccagcaccgg gctgcgctta tcgcgagggg cacaaacggt 2160
63 gagtggtctg tggatgctct gtacgggaag gtccctgacgg atgagcagta ccaggcagtg 2220
64 cgggcccagc ccaccaaccc aagcaagatg cggaagctct tcagtttcac accagcctgg 2280
65 aactggacct gcaaggactt gtcctccag gccctaagg agtcccagtc ctacctggtg 2340
66 gaggacctgg agcggagctg aggcctcttc ccagcaacac tccggtcagc cctgggcaat 2400
67 cccaccaaat catcctgaat ctgatctttt tatacacaat atacgaaaag ccagcttgaa 2460
68 cttgtgtgtt ttctgcttc tagcctgctg gcatgtgcag agctcagcta tgcttcagag 2520
69 gccacccagc ctccagctcc atgtccctag ggtctctggc accccaaatg cttcccccat 2580
70 ccttctggt atcgccatgg aatatecctc ctcattcacc aggtggtgct cctccagtgc 2640
71 tccctaaaag gtctaacctt accattatag ataacagcct gtgacccagg tccggaaggt 2700
72 aaaagaggca tgtaccaaag ggcgcaaaact ggtgggcagc tctgtccaag ccatttagaa 2760
73 acacactagt cttcatagct cccctacctt ccacattttc cactggaaga aaaaatggca 2820
74 a 2821

76 <210> SEQ ID NO: 2
77 <211> LENGTH: 770
78 <212> TYPE: DNA
79 <213> ORGANISM: Homo Sapiens
81 <220> FEATURE:
82 <221> NAME/KEY: CDS
83 <222> LOCATION: (75)...(662)
85 <400> SEQUENCE: 2
86 ccacgcgtcc gacttctctc tggctggcgg ctgcagcggg gtgagcggcg gcagcggcgg 60
87 gggatcctgg agcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg 110
88 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu
89 1 5 10
91 gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg 158
92 Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu
93 15 20 25
95 tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg 206
96 Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
97 30 35 40
99 ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac 254
100 Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
101 45 50 55 60
103 ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg 302
104 Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met
105 65 70 75
107 ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc 350
108 Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly
109 80 85 90
111 tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca gcc 398
112 Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala
113 95 100 105
115 aag cca ggc ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg 446
116 Lys Pro Gly Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala
117 110 115 120
119 agg gtc aca aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc 494

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120 Arg Val Thr Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val
121 125 130 135 140
123 ctg acg gat gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca 542
124 Leu Thr Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro
125 145 150 155
127 agc aag atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc 590
128 Ser Lys Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr
129 160 165 170
131 tgc aag gac ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg 638
132 Cys Lys Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu
133 175 180 185
135 gtg gag gac ctg gag cgg agc tga ggctccttcc cagcaacact ccggtcagcc 692
136 Val Glu Asp Leu Glu Arg Ser *
137 190 195
139 cctggcaatc ccaccaaata atcctgaatc tgatcttttt atacacaata tacgaaaagc 752
140 cagcttgaaa aaaaaaaaaa 770
142 <210> SEQ ID NO: 3
143 <211> LENGTH: 195
144 <212> TYPE: PRT
145 <213> ORGANISM: Homo Sapiens
147 <400> SEQUENCE: 3
148 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
149 1 5 10 15
150 Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu
151 20 25 30
152 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
153 35 40 45
154 Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
155 50 55 60
156 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
157 65 70 75 80
158 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala
159 85 90 95
160 Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu
161 100 105 110
162 His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn
163 115 120 125
164 Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu
165 130 135 140
166 Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg
167 145 150 155 160
168 Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu
169 165 170 175
170 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu
171 180 185 190
172 Glu Arg Ser
173 195
175 <210> SEQ ID NO: 4
176 <211> LENGTH: 626

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177 <212> TYPE: DNA
178 <213> ORGANISM: Homo Sapiens
180 <400> SEQUENCE: 4
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182 aaggcgggga gtccaggttc cgccccggag ccgacttctt cctggtcggc ggctgcagcg      120
183 gggtagcgcg cggcagcgcg cggggatcct ggagccatgg ggcgcgcgcg cgacgccatc      180
184 ctggatgcgc tggagaacct gaccgcggag gagctcaaga agttcaagct gaagctgctg      240
185 tcggtgccgc tgcgcgaggg ctacgggcgc atccgcggg gcgcgctgct gtccatggac      300
186 gccttggacc tcaccgacaa gctggtcagc ttctacctgg agacctacgg cgccgagctc      360
187 accgctaacg tgcgcgcga catgggcctg caggagatgg ccgggcagct gcaggcggcc      420
188 acgcaccagg gtgagccgcc cccgttcccc tccaccctgt ctttccctc caccacacc      480
189 agcgcttacc ccgcgggctc ttccgcttcc tgttctctct acccctaaac aaagctgctc      540
190 taccggaaag gaggctcccc acgcttgccc taccgaccaa cgggaccctg gccccacggc      600
191 ggggaaggaa ggggaaggga tcactt                                     626
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 340
195 <212> TYPE: DNA
196 <213> ORGANISM: Homo Sapiens
198 <220> FEATURE:
199 <221> NAME/KEY: CDS
200 <222> LOCATION: (67)...(339)
202 <400> SEQUENCE: 5
203 ccgacttctt cctggtcggc ggctgcagcg gggtagcgcg cggcagcgcg cggggatcct      60
204 ggagcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg gag aac      108
205      Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn
206      1          5          10
208 ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg tgc gtg      156
209 Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val
210 15          20          25          30
212 ccg ctg cgc gag gcc tac ggg cgc atc ccg cgg gcc gcg ctg ctg tcc      204
213 Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser
214          35          40          45
216 atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac ctg gag      252
217 Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu
218          50          55          60
220 acc tac gcc gcc gag ctc acc gct aac gtg ctg cgc gac atg ggc ctg      300
221 Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu
222          65          70          75
224 cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag g      340
225 Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln
226          80          85          90
229 <210> SEQ ID NO: 6
230 <211> LENGTH: 91
231 <212> TYPE: PRT
232 <213> ORGANISM: Homo Sapiens
234 <400> SEQUENCE: 6
235 Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
236 1          5          10          15
237 Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu

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238          20          25          30
239 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
240          35          40          45
241 Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
242          50          55          60
243 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
244          65          70          75          80
245 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln
246          85          90
248 <210> SEQ ID NO: 7
249 <211> LENGTH: 57
250 <212> TYPE: DNA
251 <213> ORGANISM: Homo Sapiens
253 <220> FEATURE:
254 <221> NAME/KEY: CDS
255 <222> LOCATION: (3)...(56)
257 <400> SEQUENCE: 7
258 gc tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca      47
259 Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala
260 1 5 10 15
262 gcc aag cca g      57
263 Ala Lys Pro
267 <210> SEQ ID NO: 8
268 <211> LENGTH: 18
269 <212> TYPE: PRT
270 <213> ORGANISM: Homo Sapiens
272 <400> SEQUENCE: 8
273 Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala
274 1 5 10 15
275 Lys Pro
278 <210> SEQ ID NO: 9
279 <211> LENGTH: 356
280 <212> TYPE: DNA
281 <213> ORGANISM: Homo Sapiens
283 <220> FEATURE:
284 <221> NAME/KEY: CDS
285 <222> LOCATION: (3)...(258)
287 <400> SEQUENCE: 9
288 gc ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg agg gtc      47
289 Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val
290 1 5 10 15
292 aca aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc ctg acg      95
293 Thr Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr
294 20 25 30
296 gat gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca agc aag      143
297 Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys
298 35 40 45
300 atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc tgc aag      191
301 Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys

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FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\E03557003NEW.TXT

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L:309 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 9
L:530 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:530 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
L:581 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:581 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:581 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23